

Package ‘haploR’

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Type Package

Title Query HaploReg and RegulomeDB

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Description A set of utilities for querying

HaploReg <<http://archive.broadinstitute.org/mammals/haploreg/haploreg.php>>
and RegulomeDB <<http://www.regulomedb.org>> web-based tools. The package connects to Haploreg or RegulomeDB, searches and downloads results, without opening web pages, directly from R environment.
Results are stored in a data frame that can be directly used in various kinds of downstream analyses.

RoxygenNote 5.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

Imports httr,XML

Depends R (>= 3.3)

Encoding UTF-8

License GPL

NeedsCompilation no

Repository CRAN

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getStudyList	<i>This function queries HaploReg web-based tool in order to see a list of GWAS.</i>
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Description

This function queries HaploReg web-based tool in order to see a list of GWAS.

Usage

```
getStudyList(url = "http://archive.broadinstitute.org/mammals/haploreg/haploreg.php")
```

Arguments

url A url to HaploReg. Default: <http://archive.broadinstitute.org/mammals/haploreg/haploreg.php>

Value

A list of studies. Each study is itself a list of two: name, id.

Examples

```
studies <- getStudyList()
studies
```

queryHaploreg	<i>This function queries HaploReg web-based tool and returns results.</i>
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Description

This function queries HaploReg web-based tool and returns results.

Usage

```
queryHaploreg(query = NULL, file = NULL, study = NULL, ldThresh = 0.8,
  ldPop = "EUR", epi = "vanilla", cons = "siphy", genotypes = "gencode",
  url = "http://archive.broadinstitute.org/mammals/haploreg/haploreg.php",
  verbose = FALSE)
```

Arguments

query	Query (a vector of rsIDs).
file	A text file (one refSNP ID per line).
study	A particular study. See function <code>getStudyList(...)</code> . Default: NULL.
ldThresh	LD threshold, r2 (select NA to only show query variants). Default: 0.8.
ldPop	1000G Phase 1 population for LD calculation. Can be: "AFR", "AMR", "ASN". Default: "EUR".
epi	Source for epigenomes. Possible values: vanilla for ChromHMM (Core 15-state model); imputed for ChromHMM (25-state model using 12 imputed marks); methyl for H3K4me1/H3K4me3 peaks; acetyl for H3K27ac/H3K9ac peaks. Default: vanilla.
cons	Mammalian conservation algorithm. Possible values: gerp for GERP, siphy for SiPhy-omega, both for both. Default: siphy.
genetypes	Show position relative to. Possible values: gencode for Gencode genes; refseq for RefSeq genes; both for both. Default: gencode.
url	HaploReg url address. Default: <code><http://archive.broadinstitute.org/mammals/haploreg/haploreg.php></code>
verbose	Verbosing output. Default: FALSE.

Value

A data frame (table) with results similar to HaploReg uses.

Examples

```
data <- queryHaploreg(c("rs10048158", "rs4791078"))
head(data)
```

queryRegulome	<i>This function queries RegulomeDB www.regulomedb.org web-based tool and returns results in a data frame.</i>
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Description

This function queries RegulomeDB www.regulomedb.org web-based tool and returns results in a data frame.

Usage

```
queryRegulome(query = NULL, format = "full",
  url = "http://www.regulomedb.org/results", verbose = FALSE)
```

Arguments

<code>query</code>	Query (a vector of rsIDs).
<code>format</code>	An output format. Only <code>full</code> is currently supported.
<code>url</code>	Regulome url address. Default: <code><http://www.regulomedb.org/results></code>
<code>verbose</code>	Verbosing output. Default: <code>FALSE</code> .

Value

A list of two: (1) a data frame (table) and (2) a list of bad SNP IDs. Bad SNP ID are those IDs that were not found in 1000 Genomes Phase 1 data

Examples

```
data <- queryRegulome(c("rs4791078", "rs10048158"))
head(data[["res.table"]])
head(data[["bad.snp.id"]])
```

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